

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 164801

TO: Celine Qian
Location: REM 2A64
Art Unit: 1636
Wednesday, September 07, 2005

2070

Case Serial Number: 09/913878

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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18 77N: Ed Hart

Access DB# 164801

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Celine Qian Examiner # 78710 Date: 9/6/05
Art Unit: 1636 Phone Number 302 20777 Serial Number: 09/913878
Mail Box and Bldg/Room Location: 2A 64 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Isolation & characterization of a n. crassa silencing
Inventors (please provide full names): Giuseppe et al.

Earliest Priority Filing Date: 2/16/2000

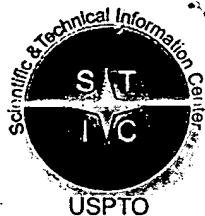
For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search nt 2447-6652 bp. of SEQ ID NO:1.
(interference only).

STAFF USE ONLY

Type of Search		Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>9/6/05</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>9/7/05</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep. Review Time: _____	Fulltext _____	Sequence Systems <u>21</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher* or *contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2005, 12:28:46 ; Search time 646 Seconds
(without alignments)
10653.529 Million cell updates/sec

Title: US-09-913-878A-1_COPY_2447_6652

Perfect score: 4206

Sequence: 1 atgagaccctactctctctag.....tcacagggaatggcattat 4206

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/6C_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfillseq.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51.6	1.2	1164	1	US-07-640-476-6 Sequence 6, Appl
2	49	1.2	3731	3	US-08-811-583-1 Sequence 1, Appl
3	44	1.0	1318	3	US-08-986-304-1 Sequence 1, Appl
4	41	1.0	1929	4	US-09-902-540-9129 Sequence 9129, Ap
5	41	1.0	10216	4	US-09-902-540-976 Sequence 976, App
6	40.8	1.0	4403765	3	US-09-103-840A-2 Sequence 2, Appl
7	40.8	1.0	4411529	3	US-09-103-840A-1 Sequence 1, Appl
8	40.2	1.0	803	4	US-09-270-767-12025 Sequence 12025, A
9	39.6	0.9	1209	4	US-09-107-532A-1706 Sequence 1706, Ap
10	39.6	0.9	1509	4	US-09-252-991A-12165 Sequence 12165, A
11	39.6	0.9	1692	4	US-09-252-991A-12425 Sequence 12425, A
12	38.8	0.9	7218	1	US-08-232-463-14 Sequence 14, Appl
13	38.6	0.9	3192	4	US-09-949-016-2923 Sequence 2923, Ap
14	38.6	0.9	3489	4	US-09-949-016-2922 Sequence 2922, Ap
15	38.6	0.9	36093	4	US-09-949-016-14664 Sequence 14664, A
16	38.6	0.9	36093	4	US-09-949-016-14665 Sequence 14665, A
17	38	0.9	17897	4	US-09-902-540-1182 Sequence 1182, Ap
18	37.2	0.9	505	4	US-09-621-976-15639 Sequence 15639, A
19	36.8	0.9	1548	2	US-08-762-106-5 Sequence 5, Appl
20	36.8	0.9	1548	2	US-09-320-774-5 Sequence 5, Appl
21	36.8	0.9	1581	2	US-08-762-106-6 Sequence 6, Appl
22	36.8	0.9	1581	2	US-09-320-774-6 Sequence 6, Appl
23	36.8	0.9	2182	4	US-09-270-767-13530 Sequence 13530, A
24	36.6	0.9	1065	4	US-09-340-798A-31 Sequence 31, Appl
25	36.6	0.9	1160	4	US-09-023-655-909 Sequence 909, App
26	36.2	0.9	816	4	US-09-252-991A-11434 Sequence 11434, A
27	36.2	0.9	1332	4	US-09-252-991A-14685 Sequence 14685, Ap

28	36.2	0.9	1473	4	US-09-252-991A-4812 Sequence 4812, Ap
29	36.2	0.9	1524	4	US-09-252-991A-11455 Sequence 11455, A
30	36.2	0.9	1551	4	US-09-252-991A-4758 Sequence 4758, Ap
31	36.2	0.9	2028	4	US-09-252-991A-11416 Sequence 11416, A
32	35.4	0.8	1437	4	US-09-902-540-8578 Sequence 8578, Ap
33	35.4	0.8	1722	3	US-09-385-028-15 Sequence 15, Appl
34	35.4	0.8	1722	4	US-09-726-614-15 Sequence 15, Appl
35	35.4	0.8	1722	4	US-09-385-040-15 Sequence 15, Appl
36	35.4	0.8	9081	4	US-09-902-540-905 Sequence 905, Appl
37	35.4	0.8	11604	3	US-09-385-028-13 Sequence 13, Appl
38	35.4	0.8	11604	4	US-09-726-614-13 Sequence 13, Appl
39	35.4	0.8	11604	4	US-09-385-040-13 Sequence 13, Appl
40	35.4	0.8	15079	3	US-09-385-028-11 Sequence 11, Appl
41	35.4	0.8	15079	4	US-09-726-614-11 Sequence 11, Appl
42	35.4	0.8	15120	4	US-09-385-040-11 Sequence 11, Appl
43	35.2	0.8	1546	3	US-09-383-318A-1 Sequence 1, Appl
44	35.2	0.8	3711	4	US-09-902-540-7049 Sequence 7049, Ap
45	35.2	0.8	13624	4	US-09-902-540-1053 Sequence 1053, Ap

ALIGNMENTS

RESULT 1
US-07-640-476-6
Sequence 6, Application US/07640476
Patent No. 5376536
GENERAL INFORMATION:
APPLICANT: QUAX, WILHELMUS
APPLICANT: LUTTEN, RUDOLF G.M.
APPLICANT: SCHUBHUIZEN, PAUL W.
APPLICANT: MRABET, NADIR
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,476
FILING DATE: 19910110
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptomyces murinus
STRAIN: DSM 40091
FEATURE:

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/ NAME/KEY: CDS
/ LOCATION: 1..1164
/ IDENTIFICATION METHOD: experimental
/ OTHER INFORMATION: /BC_number= 5.3.1.5
/ OTHER INFORMATION: /product= "xylose isomerase (glucose isomerase)"
/ OTHER INFORMATION: /evidence= EXPERIMENTAL
/ OTHER INFORMATION: /standard_name= "D-xylose ketol isomerase"
US-07-640-476-6
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Query Match 1.2%; Score 51.6; DB 1; Length 1164;
Best Local Similarity 47.8%; Pred. No. 2.5e-05;
Matches 150; Conservative 0; Mismatches 164; Indels 0; Gaps 0;
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QY 31 AGCCCCGTCGAGGAATATCAATTAACCGGCTCATATACAGTCAACCTGGGCTCCAGTGT 90
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Db 16 ACCCCCGAGAGACAGTTCACCTTCGTGTGTGACCTGTGGCGAGGAGAGACCCG 75
QY 91 GTGCGACAGACAACTCTGACCCGCCACCGCGGAGAGCTGGCCGAGATGACGAGAT 150
    |||||
Db 76 TTGCGGACGACGACCGGCCCGCTGACCGGATGAGAGGAGGAGGCGGCTGGCCGAG 135
QY 151 TTGGTGTCCATGACAAAGATCTACAGAGCCCTGAATCTTCTTACTGGCGGAGAGATGAC 210
    |||||
Db 136 CTGGGGGCTTACGAGTGTGACCTTTCACGACGACGACCTGATCCCTTGGGCTCTCCGAC 195
QY 211 TCCCTGAACGAGGACAGAGCCAACTTCTTCATGAGGCGCAAGCTGCGAGCTGAACTGG 270
    |||||
Db 196 ACCGAGGCGCAGTGTGACATCAAGCGCTTCCGCGACGCGCTGAGACCGCACCGCATGAGC 255
QY 271 GTGCCCCAAGCCACGCGGACCTGACACGCTTCCGTGTGCAAGAACTCCCGCGCC 330
    |||||
Db 256 GTGCCCCATGGCCACACCAACTCTTCAACCCACCGCTTCAAGAGCGGCGCTTACCC 315
QY 331 GCTACTGCGGCGCA 344
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Db 316 GCCAAGACCGCGCA 329
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RESULT 2

```
US-08-811-583-1
/ Sequence 1, Application US/08811583
```

```
/ Patent No. 6218142
/ GENERAL INFORMATION:
/ APPLICANT: Maseneger, Michael
/ APPLICANT: Riedel, Leonard
/ APPLICANT: Schiebel, Winfried
/ APPLICANT: Sanger, Heinz
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
/ TITLE OF INVENTION: POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
/ TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RDRP)
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FISH & NEAVE
/ STREET: 1251 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10020
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/811,583
/ FILING DATE: 05-MAR-1997
/ CLASSIFICATION: 536
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley, James F.
/ REGISTRATION NUMBER: 27,794
/ REFERENCE/DOCKET NUMBER: MPG-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-596-9000
```

```
/ TELEFAX: 212-596-9090
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 3731 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ ORIGINAL SOURCE:
/ ORGANISM: Tomato
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 194..3535
US-08-811-583-1
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Query Match 1.2%; Score 49; DB 3; Length 3731;
Best Local Similarity 51.6%; Pred. No. 0.00041;
Matches 112; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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QY 2850 TACACTCCTATGGACTGTGATGTCCTGTGGCGGAGATCCCGACCAATTCCTAGTGA 2909
    |||||
Db 2425 TAATTTCAATTCGAAAGGAAATGTGTTGTTCAAAAATCCATGCTTGATCTGGTGA 2484
QY 2910 TATCCAAAGGTTGAGCAGTCTTCAAGCAGAGCTCCACATCTCAAGAGATGTAATCAT 2969
    |||||
Db 2485 TATTCGTGTTTAAAGGCTGTAAATGTTGAGCGCTGACCAACATGTAGATGTGTGT 2544
QY 2970 CTCTCTACTAAGAGATGTACCGCTTCTTAAGAGCTATGTGTGAGACTAGACAGG 3029
    |||||
Db 2545 ATTCCTCTGAAAGAAAGAAAGACCTCATCCGAATGATGTCTGTGAGATGTGATGG 2604
QY 3030 CGATATGGCGCTGGTCTGCTGGATCCGAGATCGTC 3066
    |||||
Db 2605 GGATATCTACTTGTGTTGCTGGGATCAAGACATGATC 2641
    |||||
```

RESULT 3

```
US-08-986-304-1
/ Sequence 1, Application US/08986304A
```

```
/ Patent No. 6184343
/ GENERAL INFORMATION:
/ APPLICANT: Stamatoyanopoulos, George
/ APPLICANT: Papayannopoulou, Thalia
/ APPLICANT: Yang, Yi
/ TITLE OF INVENTION: FETAL GLOBIN INDUCING FACTOR
/ FILE REFERENCE: 64657.0102
/ CURRENT APPLICATION NUMBER: US/08/986,304A
/ CURRENT FILING DATE: 1997-12-05
/ EARLIER APPLICATION NUMBER: 60/033,247
/ EARLIER FILING DATE: 1996-12-06
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1318
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-08-986-304-1
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Query Match 1.0%; Score 44; DB 3; Length 1318;
Best Local Similarity 51.0%; Pred. No. 0.0078;
Matches 104; Conservative 0; Mismatches 100; Indels 0; Gaps 0;
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QY 2506 AATCGCCGAGTGAATTTGCGCAATGGGTTTACGAGATTTATTCAGTGGCGCACTGGA 2565
    |||||
Db 592 AATACAGAGTGAGCTTCTTTCTTACTGACGATGTGACATATATATGCCAATCAAAA 651
QY 2566 GTCAAGCAGCGCGGTGTGCTTTCTTGTGGCTTACCTGACAGTCAAGAGAGCACTG 2625
    |||||
Db 652 GGCCTCTTGACCCCTTGATCTTGTGTGGGACAGAGACAGCAAGATACCTTAGAA 711
QY 2626 AACTCTTGATGAACAGTGGGTTGATCCCAAGAAAGAAAGTACTTGCAAGACATCGCC 2685
    |||||
Db 712 CTCCTCTGATGAACCGTTACGTCAACACAGGCTGAAACAACTTGGAAGAACTGCA 771
    |||||
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QY	2686	TGGGATCTTCAAAAGCGGAATGT	2709
Db	772	TTTGATATTGCCAGGAGACAAGT	795

RESULT 4
US-09-902-540-9129

```

: Sequence 9129, Application US/09902540
: Patent No. 6833447
:
: GENERAL INFORMATION:
:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(15849)B
:
: CURRENT APPLICATION NUMBER: US/09/902,540
:
: CURRENT FILING DATE: 2001-07-10
:
: PRIOR APPLICATION NUMBER: 60/217,883
:
: PRIOR FILING DATE: 2000-07-10
:
: NUMBER OF SEQ ID NOS: 16825
:
: SEQ ID NO 9129
:
: LENGTH: 1929
:
: TYPE: DNA
:
: ORGANISM: Myxococcus xanthus
:
: US-09-902-540-9129

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Query Match	1.0%	Score 41	DB 4	Length 1929
Best Local Similarity	47.2%	Pred. No. 0.097		
Matches 125; Conservative	0	Mismatches 140	Indels 0	Gaps 0

Dd		692	AGAAACAACCTGGCGGAATCACTGACGCCCATCGAGANTCGAAGAAGCGCACACCCGCA	751
Qy		3587	CTCACTTTTGGGAAATCCGATCTCGCTTCTTAATACTACGTTCTTCAAAGAGATTAGCGACA	3648
Dd		752	AGCTGGGCMAAGAACCTGGACTGTGACCTTCTCCACTCCCTTACTTCGCGCGGCTCCGCTTCT	811
Qy		3647	AGTCGCGATCGTCGCGCACTGCTATTCAACGATCTGMAAACCATTACGGCGAAGTCGAGA	3706
Dd		812	GGAACCCCAGAAAGGACCAACGCTCTTACACCAACGCTGTGAACTGGATGGCTCAGCTGACGC	871
Qy		3707	AAGAATATGGCAGGTTGCTCAAAAACAAGAGATAGAGACAGCAAGGACCCCTAACCTTG	3766
Dd		872	AGAACGACGCGCTACGTGGAGATCAAGAAGCCCCCTGATGTTCAACAAAGGGGCTGTGGAGA	931
Qy		3767	TTCGCGTCAACCAAGTTTATGAAAA	3791
Dd		932	CCAGCGGCGCACTGAGGCGCAATGACA	956

RESULT 5
US-09-902-540-976/c

```

? Sequence 976, Application US/00902540
? Patent No. 6833447
? GENERAL INFORMATION:
? APPLICANT: Goldman, Barry S.
? APPLICANT: Goldman, Gregory J.
? APPLICANT: Hinkle, Gregory J.
? APPLICANT: Slater, Steven C.
? APPLICANT: Wiegand, Roger C.
? TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
? FILE REFERENCE: 38-10(15849)B
? CURRENT APPLICATION NUMBER: US/09/902,540
? CURRENT FILING DATE: 2001-07-10
? PRIOR APPLICATION NUMBER: 60/217,883
? PRIOR FILING DATE: 2000-07-10
? NUMBER OF SEQ ID NOS: 16825
? SEQ ID NO 976
? LENGTH: 10216
? TYPE: DNA
? ORGANISM: Myxococcus xanthus

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US-09-902-540-976

Query Match	1.0%;	Score 41;	DB 4;	Length 10216;
Best Local Similarity	47.2%;	Pred. No. 0.34;		
Matches 125; Conservative	0;	Mismatches 140;	Indels 0;	Gaps 0

QY	3527	ACAAGAACTCGAAGCCCTTCCACAAATCCATGAAAGCGCCAAAGATACAGAAACGCG	3586
Db	2066	AGAAACAACCTGGGAGATCACTGACCGGCATTCAGAGAGTGGAAGAAACGGGACCAACGCA	20077
QY	3587	CTCACTTTGGGAACTCGGATCTCGCTTCTTCACTACACGTTCTTTCAGAGAGATTAGCGACA	36486
Db	2006	AGCTGGGCAAGAGACTGAGACCTTTCACATTTCCACCCGTACTCGCCGGCTCCGCTTCT	19478
QY	3647	AGTCGGATGTCGTCGCACTGCTATTACGACTGTGAAGAAACCGATGCGGAGATCGAGA	37060
Db	1946	GGACCCCGAAGGGCACACGCTTCAACACAGCTGTGAACTGGATCGTTCAGCTGACGC	18877
QY	3707	AAGATTATGCGCAGGTGTCCTCAAAAACAGAGATGAGAGACAGCAAGACCCCTTACCCTG	37665
Db	1886	AGAAACGACGCTACGTGAGATCAAGACGCCCTGATGTTCAACAAGGGCTGTGGGAGA	18237
QY	3767	TCCGCGTCAACAGGTTTATGAAAA	3791
Db	1826	CCAGCGGCACTGGGGCAGATTACA	1802

RESULT 6

```

US-09-103-840A-2
? Sequence 2, Application US/09103840A
? Patent No. 6294328
? GENERAL INFORMATION:
? APPLICANT: FLEISCHMAN, Robert D.
? APPLICANT: WHITE, Owen R.
? APPLICANT: FRASER, Claire M.
? TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
? TITLE OF INVENTION: TUBERCULOSIS
? FILE REFERENCE: 24366-20007.00
? CURRENT APPLICATION NUMBER: US/09/103,840A
? CURRENT FILING DATE: 1998-06-24
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 2
? LENGTH: 4403765
? TYPE: DNA
? ORGANISM: Mycobacterium tuberculosis
? FEATURE:
? OTHER INFORMATION: CDC 1551
? OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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Query Match	1.0%;	Score 40.8;	DB 3;	Length 4403765;
Best Local Similarity	49.5%;	Pred. No. 37;		
Matches 105; Conservative	0;	Mismatches 107;	Indels 0;	Gaps 0;

Qy	3952	CCCAAGTTGATGTGGCAGATGGCCGGGACAGACGTCCGGTTCATTAAAGGCGCAGATACG	4011
Db	426833	CCCGAATTGTGTCCGCCGATGCCCACTCTGGCTGTGCGCGGATAGGCCGACCGCGAAACCG	426897
Qy	4012	AGCAGACCCGGATGAAGGCGCCCGCGCTGTGATGACCGCGTTCATGTATGCGGCGCTTGATG	4071
Db	426893	CCGGTATCCCATGTGTCCGATGCCGACGTTGCGCGGTGCCGAGTTGAACAAGCCGGTGTG	426957
Qy	4072	CCCGATTAGAAATTTCAGAACGATATGTGGCCAGGCTGGAGGGCGATGATCGAGTAC	4131
Db	426953	CCGGTCCCGGATTGTGACAAACCCGGTGTGTGCGGTGCCGAGTTGAAGAAACCCGTTG	427012
Qy	4132	CCGTGATCCGGAGGCTTATGAAGTGTGGGCGA	4163
Db	427013	CCGGCGCCGGAATTACGGAGCTGAAGCCGGA	427044

```
RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match 1.0%; Score 40.8; DB 3; Length 4411529;
Best Local Similarity 49.5%; Pred. No. 37;
Matches 105; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 3952 CCCAAGTTCGTGTGGCAGATGGCGGCGACAGCAGCTCCGCTACATTAAAGCGCGCATGACG 4011
    |||||
DB 426675 CCGAGATTGTGTCCGCGCGGACCACTGTGCTGCGCGGATGAGCGCGGACCGCGG 426734
    |||||
QY 4012 AGCAGACCCGGTGAAGGCGCCGCGCGTGTATGACCGCTTCACTGTATGCGGGCTTGATG 4071
    |||||
DB 426735 CCGGTGCCCATGTTCCGAGATCCGACCTTCCGCTGCCAGATTGAACAGCCGGTGTTG 426794
    |||||
QY 4072 CCGGATTAAGATTATTCAGAACAGATATGTGCGCCAGCTGTGAGGCGCGATGATGAGATAC 4131
    |||||
DB 426795 CCGGTGCGGAGTTGAACCAACCGGTGTGTGGCGGTGCGGAGTTGAAGAAACCGGTGTTG 426854
    |||||
QY 4132 CCGATCCGAGAGGTCTATGAAAGTCTGTGGGCGA 4163
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DB 426855 CCGGCGCGGAGTTCAAGGAGCTGAAGCCGGA 426886
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RESULT 8
US-09-270-767-12025/C
; Sequence 12025, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12025
; LENGTH: 803
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12025
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Query Match 1.0%; Score 40.2; DB 4; Length 803;
Best Local Similarity 70.1%; Pred. No. 0.091;
Matches 55; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 4109 TGAAGGCGATGATCGAGATACCTGTATCGAGGTCTATGAAGTGTGGCGCATGATG 4168
    |||||
DB 96 TGAAGGCGATGATCGAGGTGTGGCCCATGTGTGGAGGTGCATGTGTGTGTGGCCCATGATG 37
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QY 4169 ATTATGATGAATTTGCT 4185
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Db 36 ATGTGTGTGTGTGTGTGT 20

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RESULT 9
US-09-107-532A-1706
; Sequence 1706, Application US/09107532A
; Patent No. 6563275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Dencke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1706:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1209 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...1209
; SEQUENCE DESCRIPTION: SEQ ID NO: 1706:
US-09-107-532A-1706
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Query Match 0.9%; Score 39.6; DB 4; Length 1209;
Best Local Similarity 49.1%; Pred. No. 0.19;
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 2504 TGAATCGCCAGTGAATTTGCCCAATGGGTTTACAGAGATTATTCAGTCGCCGAACTC 2563
    |||||
DB 386 TGATTGATCTGTGGAATGGCCCGTGAGATGTTAGATGCTAACCCACATGAATATCTG 445
    |||||
QY 2564 GAGTCAGCCAGCGCGGTGTCTTTTCTTGCTGTGGCTACTGACGTCAAGAGAGACAC 2623
    |||||
DB 446 GTGTGACGACGAGCGTATTTGAGTGTCTGCGCCCTTGACGCGAATCAAGATATCATCT 505
    |||||
QY 2624 TGAATCTTTTGAAGACAGTGGTGTGATCCCAAGAGAAAGTACTTGAAGACATCG 2683
    |||||
DB 506 TGATGACGACGACATTCGGTGTGCTTGATCCAAATCATCTGTGATTCCTTGGACAGCCTTG 565
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QY 2684 CCGGATCTTCAAAAAGCGAATGTGACACGTT 2717
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Db 566 TCAAGATTACAGAGCGTTTGGGAAAAACGAT 599

RESULT 10
US-09-252-991A-12165
; Sequence 12165, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12165
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12165

Query Match 0.9%; Score 39.6; DB 4; Length 1509;
Best Local Similarity 45.3%; Pred. No. 0.23;
Matches 144; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 3638 TTAGCGACAAGTCGCGCATGCTGCTATTCAGACCTGGAAGACCGTATCGGCG 3697
Db 482 TCACCCGCGAAGAGTCCACCGAGGCGCTGCTGCTGCGGACATCTCCGCGCG 541
QY 3698 AAGTCGAGAAAGATATGAGGCTGCTCAAAAACAAGAGATGAGACAGCAAGGACC 3757
Db 542 ATGTCGAGATTCGCTGGATGCGATGAGCATGAGGCTGCTGAGGCGGACGCGCTGC 601
QY 3758 CCTACCTGTCCGCGTCAACAGCTTATGAAAAATGTCGCCATACCGCTGAGGCGCA 3817
Db 602 CCACCTACTTCTCCGCGCAAGTGGTGCACACCACTGATGGGCATCACCCAGCTCTGC 661
QY 3818 TGACAAATCCGAGCAATATGATCTAAGGATCAGGTTGCTGGAGCTGTCTCC 3877
Db 662 GCGCGGAGAGTGTCTGCTGCGCGCCCAAGCTGATCAAGCTTACAGATATTTGCGCT 721
QY 3878 TCGCGGACCGTGAATGATGAGGATGCGCATTTGCTGAGGCGCTAGACGCGCTTCAAGCTGT 3937
Db 722 GGGAGGACCGGAGCTGTGTCTACATGCGCATGCTGGCGCAACCGGACAAAGCAAGCTGT 781
QY 3938 ACTACCAAGAGCGCCCA 3955
Db 782 CCAAGCGCAAGATCCGA 799

RESULT 11
US-09-252-991A-12425/c
; Sequence 12425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR APPLICATION NUMBER: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12425
; LENGTH: 1692

; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12425

Query Match 0.9%; Score 39.6; DB 4; Length 1692;
Best Local Similarity 45.3%; Pred. No. 0.25;
Matches 144; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 3638 TTAGCGACAAGTCGCGCATGCTGCTATTCAGACCTGGAAGACCGTATCGGCG 3697
Db 1124 TCACCCGCGAAGAGTCCACCGAGGCGCTGCTGCTGCGGACATGCTCCGCGCG 1065
QY 3698 AAGTCGAGAAAGATATGAGGCTGCTCAAAAACAAGAGATGAGACAGCAAGGACC 3757
Db 1064 ATGTCGAGATTCGCTGGATGCGATGACATGAGTGTGTAAGAGGCGGACGCGCTGC 1005
QY 3758 CCTACCTGTCCGCGTCAACAGCTTATGAAAAATGTCGCCATACGCGCTGAGGCGCA 3817
Db 1004 CCACCTACTTCTCCGCGCAAGTGGTGAAGACCACTGATGGGCAATCACCACTGCTGC 945
QY 3818 TGACAAATCCGAGCAATATGATCTAAGGATGATGAGTGTGCTGAGCTGTCTTCC 3877
Db 944 GCGCGCAAGAGTGGCTGCCGCGCGCCCAAGCTGATCAAGCTTACAGTATTTTCGGCT 885
QY 3878 TCGCGGACCGTGAATGATGATGAGGCAATGCGCTGAGGCGCTAGCAGCGCTTCAAGCTGT 3937
Db 884 GGGAGGACCGGAGCTGTGCTACATGCGCATGCTGCGCAACCGGACAAAGAGCAAGCTGT 825
QY 3938 ACTACCAAGAGCGCCCA 3955
Db 824 CCAAGCGCAAGATCCGA 807

RESULT 12
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:

LENGTH: 36093
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(36093)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14664

Query Match 0.9%; Score 38.6; DB 4; Length 36093;
Best Local Similarity 52.9%; Pred. No. 5.3;
Matches 83; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 24 GAGGAATAGCCCGTCGAGGAAATCATPAACCGGCTCATATACGACTTACAACTGGGCT 83
DB 16851 GATGAGCAGCCTTATCAAGTGACTGAGTGCGACAGACATACCTTACGACTGGGTAT 16910
QY 84 CCAAGTGTGTCGACAGACAACTCTCACCCGCCGGAAGGAGCTGGCCGAGAGTGA 143
DB 16911 CCACTCGGGCGCCAAACACTGCGCTCCGTCAGCAGCAGGGCATCATGGAGAGGA 16970
QY 144 CGAGGATTTGGTGGCCATGACAAGATCTACAGAGCC 180
DB 16971 TGAGGCTTGGGGGCCAGTACGCTCAAGAAAACC 17007

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Job time : 667 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 6, 2005, 16:40:35 ; Search time 2488 Seconds

(without alignments)
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Sequence: 1 atgaacccttctctctag.....tcacaggagatgcatat 4206

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 327445616 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 23: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	1.2	3731	9	US-09-782-874-1
2	47	1.1	1164	15	US-10-156-761-7161
3	47	1.1	9025608	15	US-10-156-761-1
4	45.6	1.1	495	10	US-09-918-995-3407
5	44.8	1.1	1049	14	US-10-123-155-358
6	44.8	1.1	1049	15	US-10-146-731-358
7	44.8	1.1	1049	15	US-10-140-472-358

C 8	44.8	1.1	1049	15	US-10-141-761-358	Sequence 358, App
C 9	44.8	1.1	1049	16	US-10-142-885-358	Sequence 358, App
C 10	44.8	1.1	1049	16	US-10-158-720-358	Sequence 358, App
C 11	44.8	1.1	1049	17	US-10-137-871-358	Sequence 358, App
C 12	44.8	1.1	1049	17	US-10-140-923-358	Sequence 358, App
C 13	44.8	1.1	1049	17	US-10-141-756-358	Sequence 358, App
C 14	44.8	1.1	1049	17	US-10-141-759-358	Sequence 358, App
C 15	44.8	1.1	1049	17	US-10-140-805-358	Sequence 358, App
C 16	44.8	1.1	1049	17	US-10-140-884-358	Sequence 358, App
C 17	44.8	1.1	1049	18	US-10-142-426-358	Sequence 358, App
C 18	44.2	1.1	152165	20	US-10-719-993-6942	Sequence 6942, App
C 19	44.2	1.1	152165	21	US-10-741-600-17864	Sequence 17864, App
C 20	44.2	1.1	1980090	20	US-10-719-993-6815	Sequence 6815, App
C 21	44.2	1.1	1980090	21	US-10-741-600-17676	Sequence 17676, App
C 22	44	1.0	282	9	US-09-294-0938-1147	Sequence 1147, App
C 23	44	1.0	1540	9	US-09-925-299-62	Sequence 62, App1
C 24	44	1.0	1540	10	US-09-925-299-62	Sequence 903, App1
C 25	44	1.0	1555	15	US-10-106-698-903	Sequence 113012, App
C 26	44	1.0	1525	20	US-10-425-115-113012	Sequence 24716, App
C 27	44	1.0	1959	20	US-10-357-930-24716	Sequence 1222, App
C 28	44	1.0	94330	13	US-10-087-132-1222	Sequence 5115, App
C 29	43.8	1.0	1338	15	US-10-156-761-5115	Sequence 20636, App
C 30	43.4	1.0	3719	19	US-10-437-963-33098	Sequence 33098, App
C 31	42.6	1.0	1398	19	US-10-437-963-33098	Sequence 20619, App
C 32	42.4	1.0	506	16	US-10-029-386-20619	Sequence 23441, App
C 33	42.4	1.0	582	19	US-10-767-701-23441	Sequence 2179, App
C 34	42.4	1.0	1168	15	US-10-017-161-2179	Sequence 1825, App
C 35	42.4	1.0	1168	17	US-10-292-798-1825	Sequence 9233, App
C 36	41.2	1.0	1062	19	US-10-767-701-9233	Sequence 7803, App
C 37	41.2	1.0	1485	9	US-09-815-242-7803	Sequence 30269, App
C 38	41.2	1.0	1485	17	US-10-282-122A-30269	Sequence 545, App
C 39	41.2	1.0	1535	13	US-10-052-586-545	Sequence 545, App
C 40	41.2	1.0	1535	14	US-10-174-550-545	Sequence 545, App
C 41	41.2	1.0	1535	14	US-10-176-758-545	Sequence 545, App
C 42	41.2	1.0	1535	14	US-10-175-737-545	Sequence 545, App
C 43	41.2	1.0	1535	14	US-10-174-581-545	Sequence 545, App
C 44	41.2	1.0	1535	14	US-10-176-483-545	Sequence 545, App
C 45	41.2	1.0	1535	14	US-10-176-749-545	Sequence 545, App

ALIGNMENTS

RESULT 1
US-09-782-874-1
; Sequence 1, Application US/09782874
; Patent No. US20010023067A1
; GENERAL INFORMATION:
; APPLICANT: Messeneger, Michael
; Riedel, Leonard
; Schiedel, Winfried
; Sanger, Heinz
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
; RNA-DIRECTED RNA POLYMERASE (RDRP)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,874
; FILING DATE: 08-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/811,583
FILING DATE: 05-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Tomato
FEATURE:
NAME/KEY: CDS
LOCATION: 194..3535
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-782-874-1
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Query Match          1.2%; Score 49; DB 9; Length 3731;
Best Local Similarity 51.6%; Pred. No. 0.00041;
Matches 112; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
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DB 2425 TAATTCATCTCTGAAGGAAATGTGTGTCAAAATAATCGCTTGCAATCTGCTGATG 2484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2910 TATCCAAAGGGGTTGAGAGTCTTCAAGCAGAGCTCCACAGTCAAGATATATCAT 2969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2485 TATTCGTGTTTAAAGCTTAATGTTCAGAGCGCTGCACACATGTAATGTGTGT 2544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2970 CTCTCTACTTAAAGAGATGTACCGCTTGCTTAAAGACTATCTGTGAGACATACGACG 3029
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2545 ATTCCCTCAGAAAGAAAAGACCTCATCCGAATGATGTTCTGGAGTGATTTGGATGG 2604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3030 CGATATGCGCTGGGTCTGCTGGGATCCGGAGATCGTC 3066
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DB 2605 GGATATCTACTTGTGTTGCTGGGATCAAGACATGATC 2641
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```
RESULT 2
US-10-156-761-7161
Sequence 7161, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7161
LENGTH: 1164
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1164)
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US-10-156-761-7161
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Query Match          1.1%; Score 47; DB 15; Length 1164;
Best Local Similarity 46.9%; Pred. No. 0.00097;
Matches 146; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
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QY 31 ACCCCGTCGAGGAATCATTAACCGGCTCAATTAAGACTACACCTGGGCTCCAGTGT 90
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DB 16 ACCCCGAGGAGACAGTTTACCTTCGGCTGTGAGACCTGTGGTCAGGAAAGGACCCG 75
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 91 GTGCGACACACAATCTCTCAACCCCGACCGCGAAAGAGCTGGCCGAGAGTACGAGAT 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 76 TTGCGGAGACGACCGCGGCGCCCTTGAGACCGGTGAGACGATCAGCGCTCCCGGG 135
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 TTGCGTCCGATGACAAAGATCTACAGAGCCCTGAACCTTCTACTGTGGGGAAGATGAC 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 136 CTGCGTCCCGACGAGTGACTTTCACAGACGACGACCTGATCCCTTGCGGTCTCGGAC 195
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 211 TCCCTGAACACGACGAGAACCAACTTTCATCGAGGCCAAAGCTCGAGTCAAGTGG 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 196 ACCGAGCGGAGATCCGACATCAAGGCTTCCGCGAGGCCCTCGAGCCACCGCATGGCC 255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 GTGCCAAAGCCACGCGGACCTTGACACGCTTCGTGGTCCAGAAACCTCCCGCGC 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 256 GTGCGATGCGCACACCACTTTCAGCGCACCCGTCCTCAAGAGACGGGGCGTTACAC 315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 331 GCTACTCGCGG 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 GCCAACGACCG 326
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 3
US-10-156-761-1
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
```

```
Query Match          1.1%; Score 47; DB 15; Length 9025608;
Best Local Similarity 46.9%; Pred. No. 0.117;
Matches 146; Conservative 0; Mismatches 165; Indels 0; Gaps 0;
```

```
QY 31 ACCCCGTCGAGGAATCATTAACCGGCTCAATTAAGACTACACCTGGGCTCCAGTGT 90
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8551009 ACCCCGAGGAGACAGTTTACCTTCGGCTGTGAGACCTGTGGTCAGGAAAGGACCCG 8551068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 91 GTGCGACACACAATCTCTCAACCCCGACCGCGAAAGAGCTGGCCGAGAGTACGAGAT 150
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 8551069 TTGCGGAGACGACCGCGGCGCCCTTGAGACCGGTGAGACGATCAGCGCTCCCGGG 8551128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```



```
QY 151 TTGGTGGCCATGACAGATCTACAGAGCCCTGAACTTTCTTACTGAGCGGAAGATGAC 210
| | | | |
DB 8551129 CTGGTGTCCACGAGAGTACCTTTCACAGACGACCTGATCCCTTCTGGGTCTCTCGAC 8551188
QY 211 TTCCCTGAACGAGGAGAGGCAACTTCTTCATCGAGGCCAAAGCTGCGAGCTGAACTG 270
| | | | |
DB 8551189 ACCGAGGCGGAGTGTGACATCAACAGCGCTTCCGAGAGGCCCTTCAGACGCCACCGGATGACC 8551248
QY 271 GTGCCCCAAGCCGACGCGACCTGTACACGCTTCTGCTGTCGAAGAACTCCCGCGGCC 330
| | | | |
DB 8551249 GTGCGCGATGCGCCACCAACCACTCTTCACGACCCCGTCTTAAGAGAGCGGGGGTTTACC 8551308
QY 331 GCTACTGCGCG 341
| | | | |
DB 8551309 GCCAAGCAGCCG 8551319

RESULT 4
US-09-918-995-3407
; Sequence 3407, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918, 995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235, 076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ. ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3407
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(495)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-3407

Query Match 1.1%; Score 45.6; DB 10; Length 495;
Best Local Similarity 51.5%; Pred. No. 0.0017;
Matches 105; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 2506 AATGCCAGTGAATTTGSCAATGGGTTTACGAGGTTATTCAGTGGCGCACTCGA 2565
| | | | |
DB 287 AATACCAAGATGCTCTTCTTCTTACGACATGATGACATATCAATGCCCAACAAA 346
QY 2566 GTACGCCAGCGCGGTGCTCTTTCTTCTGCTGAGCTTACAGTCAAGAGAGACACTG 2625
| | | | |
DB 347 GGCCTCTTGACCCCTTGACCTTGTGCTGGGAAAAAGACAGCAAGTACCTTAGAA 406
QY 2626 AACTTCTTGAAGAGTGGTTCGATCCCAAGAGAAAGTACTTTCGAGACATCGCC 2685
| | | | |
DB 407 CTCCTCTGTATGACGTTAAGTCAACGAGGCTGTAAGAAACCTTGAAGAACTGCA 466
QY 2686 TGGGATCTTCAAAAGCGAAATGT 2709
| | | | |
DB 467 TTTGATATTGCCAGAGACAACT 490

RESULT 5
US-10-123-155-358/C
; Sequence 358, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyere, Luc
```

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123, 155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-123-155-358

Query Match 1.1%; Score 44.8; DB 14; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TTCCCTAACCAGGACGAGAACCACTTCTTCATCGAGGCCCAAGCGCGAGCTGAACTG 270
| | | | |
DB 1006 YMT...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTWMBK.BAAMS... 947
QY 271 GTGCCCAAGCCGACGCGCAGCTTCGAGTTCGAAGAACCTCCCGCGCC 330
| | | | |
DB 946 S.S.N..B..C..WHY..G.N.DM.Y.H.MTB..T.BM.ABT.HMAHRB..THRGH. 887
QY 331 GCTACTGCGGCGCAACATGGGCTTTCGAGTGTCTGAGTGTCTTAATAGTTT 390
| | | | |
DB 886 S..Y..RCM.MTWG.DR.RWBHW.R.DSTAKK...SBS.S.S...NA.H..GAR.H.S 827
QY 391 ATGCCACCTCCCAATPACACACAGTGAAGCTTTGGCAACTTAAGCGGCCCACT 450
| | | | |
DB 826 .SS.CMDTC.CGABAT.R..AB..ADNBWB.WBTHGAG..YND...KM..NN..BN... 767
QY 451 GGCCTGAGCGCCCAACTCTTACCAACCAAGCAAGATGAGCGCGCAATGCACT 510
| | | | |
DB 766 SAM..K..MNSS.H.RY...TH...RMA.SY..NM...SYSGNS.Y..BAA..N 709
QY 511 TTGGCTGATCGCCCAACGCTGTTGACTGCTGTGCCAGGTCTTCTTATTCAGCGC 570
| | | | |
DB 708 DS.H.A..NM.G..MMWS..SM.CNMT..S.NM.N..KCH.BCS...S.NMS.H...M.. 649
QY 571 GCGGCGATACCCCTTAAGTTCCCGATCGAGTATCCGTTCCAAAGACATCTGC 630
| | | | |
DB 648 NM...RYNHG.YW.BH.DNCY...AY.S.S..KAYSASS..HNHKK.M..BM.NMA..N. 589
QY 631 GAGAGTGAATCTCAATCATGACACCAAGCGGCGCAAGGCAAGCTGTCTATATGTT 690
| | | | |
DB 588 KDA.C.S..RDSNS.H.B..MD...THSD..H.YNS.H.RY..T....SCN.A.S. 529
QY 691 GCCGCTGCGCGCGCGCGCGCTGCTTATTCGAGCGCTTTGAGACAGTACGACTGA 750
| | | | |
DB 528 .NCS.N.GW..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK..ST.NMM.YGSYTRWH 469
QY 751 AGGCAATGCAATACAGAGATCCCAAGGAGAGATGATAGACGAGCGGACCAAGTGA 810
| | | | |
DB 468 RY.RD...B...RS.BSAYTNSG.CB..SSHCS.S.MNBS.H.BM.YM..M.KS..NT..M. 409
QY 811 TCCTTGATACATCTCAAGGCACTTCATGAGTGTGAGAGTGTCTTCAAGCGCTGCGTAC 870
| | | | |
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T..S.NKSTYRB...N. 349
```

QY 871 AATCAGAGCACTACCGAGTAGTTTGGAGCTCTCTTACAGCCCGGAGGAAGCGG 930
DB 348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A. 289
QY 931 CCTGTGATGCCAGCGCTTTGAGGCTGACACTTGATTTAGTCTCTTACGAAGAAG 990
DB 288 TH.TNB.....SNNMG.TG...TNRGY.GNCS.H.....N.NN.HH...MT.KNNR.R... 229
QY 991 ACAACCAAGTCCCACTAGATAAC 1014
DB 228 A.AS..BA.BTABNNHM.S.BM.M 205

RESULT 6

US-10-146-731-358/c
; Sequence 358, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C323
; CURRENT APPLICATION NUMBER: US/10/146,731
; CURRENT FILING DATE: 2002-05-15
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-146-731-358

Query Match 1.1%; Score 44.8; DB 15; Length 1049;

Best local Similarity 5.2%; Pred. No. 0.0049;

Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTTGAACGAGGAGGCACTTCTTCATGAGGCGCAAGCTGCGAGCTGAACCTG 270
DB 1006 YMY...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTRHAB.BAMS... 947
QY 271 GTGCCCAAGCGGCGGCGGCAAGCTTCCGTCGTCGACAGAACTCCCCCGCC 330
DB 946 S.S.N.B.C.WHY...G.N.DM.Y.H.MTB..T.BW.ABT..HMAHB..THRGH. 887
QY 331 GCTACTGCGGCGCAACATGGGCACTTGACAGCTGTGTGCTGAGGTGTTAATAGTTT 390
DB 886 S..Y.RCM.MTMG.DR.RMBHM.R.DSTAKBK...SBS.S.S...NA.H.GAR.H.S. 827
QY 391 ATGCCACCTCCCAATACACACAGAGTGAACGTTTGCGAGAACTTAAGCGGCGCAAGT 450
DB 826 .BS.CMDT.C.BGABHAT.R..AB.ADNBWB.BWTHGAG..YND..KM.NN.BN... 767
QY 451 GGCGTGAAGCGGCGGCGGCAAGCTTACCAACCAAGAGATAGCCCGGCAATGTACT 510
DB 766 SAM..K..MNS.H.RX...TH...RWA.SY..NM..NM--SYGNS.Y..BAA..N 709

QY 511 TTCGCTGATCCGCGCAAGCGCTGTGACTGCTGCGACAGAGCTCTTATTCAGCGC 570
DB 708 DS.H.A..NM.G..MMS.SM.CNMT.S.NM.N..KCH.BCS...S.SMS.H....M.. 649
QY 571 GCGGAGATACCCCTAAAGTTCCCGATCCAGTAATACGGTTCCAAAGCAATCTCTC 630
DB 648 NM...RYNHC.YW.BH.DNXY...AY.S.S.KAYSASS..HNHKK.M..BM.NMA..N. 589
QY 631 GAGAGTGAGATCTCAATCAGTCGACCAAGCGGCGCAAGCGCAAGCTGTCTATTAATG 690
DB 588 KA.C.S..RDNSS.H.B..MD...TASD..H.YNNS.H..RY..T.....SCN.A.S. 529
QY 691 GCGGTCGCGCGCGCGCGCGCTGTATTTGAGAGCGCTTTGACAAAGTACCGACTGCA 750
DB 528 .NCS.N.GM..S.D..HSMB...SNMS.H.A.CMRGS.NBSK.ST.MNM.YGSTRH 469
QY 751 AGCATGCCAATACGAGATCCACGGGCGACAGGTCAATGACGAGCGAGCGAGTGAT 810
DB 468 RY.RD...B...RS.BSAYTNSG.CB.SHCS.S.MNBS.H.BM.YM..M.KS.NT.M. 409
QY 811 TCCTTTGATACATCTCAAGCACTTCTATGTTGAGTGTCTTACGCGCTTGCCTGAC 870
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BCY.Y..M.SM.SS.T.S.NKSTYR...N. 349
QY 871 AATCAGAGCACTACCGAGTAGTTTGGAGCTCTCTTACAGCCCGGAGAGAAGCGG 930
DB 348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A. 289
QY 931 CCTGTGATGCCAGCGCTTTGAGGCTGACACTTGATTTAGTCTCTTACGAAGAAG 990
DB 288 TH.TNB.....SNNMG.TG...TNRGY.GNCS.H.....N.NN.HH...MT.KNNR.R... 229
QY 991 ACAACCAAGTCCCACTAGATAAC 1014
DB 228 A.AS..BA.BTABNNHM.S.BM.M 205

RESULT 7

US-10-140-472-358/c
; Sequence 358, Application US/10140472
; Publication No. US2003013888A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C168
; CURRENT APPLICATION NUMBER: US/10/140,472
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-472-358

Query Match 1.1%; Score 44.8; DB 15; Length 1049;

Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

```
QY 211 TCCCTGAACGAGGCAAGCACTTCTTCATGAGGCCCAAGCTCGCAACTGG 270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1006 YMY...MSM...M.....BHBH.HK.Y.DS.R.T.M.N.AMTRMHAKB.BAMMS...947

QY 271 GTGGCCAAAGCCGACGCGGACCTGACAGCGCTTCGTCGCAAGAACTCCCCCGCC 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH.887

QY 331 GCTACTGCGCGCCCAAGATGGGCAATGGGCACTGTGTGTCGAGGTGCTTAATAGTT 390
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 886 S..Y.RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S...NA.H.GAR.H.S.827

QY 391 ATGGCACTCCCATATACACACAGGTCGAACTGTGGCAAGAACTTAAGCGCCCAAGT 450
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 826 .BS.CMDTC.CBGAHAT.R..AB.ADNBMWB.WBTHGAG..YND...KM.NN.BN...767

QY 451 GCGCTGAGCGCGCCCACTCTACCAACCAAGCAAGGATGAGCCCGCCCATGTCACT 510
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 766 SAM..K..MNSH.H.RY...TH...RMA.SY..NNM...NM--SYGNS.Y..BAA..N.709

QY 511 TTGCTGATCCGCGCAAGCTGTGTAAGTCTGTCGCAAGGCTCTCTATTACGGC 570
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 708 DS.H.A..NM.G..MMMS.SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H...M..649

QY 571 GCGGCGATACCCCTTAAGTTCCCGCATCGAGTGAATACGGGTTCGAAGCAACTCTTC 630
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 648 NM...RYNHC.YW.BH.DNCY...AY.S.S.KAYSASS.HNHK.M..BM.NMA.N..589

QY 631 GAGAGTGAATCTCAATGAGTGCACCAAGCGCGCAAGGCAAGTGTCTATATGTT 690
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T....SCN.A.S..529

QY 691 GCGGTGCGCGCGCGCGCGCGCGCTGCTATGCGAGCGCTTGGACAAGTACGACTCGA 750
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK.ST.MMM.YGTYTRMH 469

QY 751 AGGCATGCCAATACAGAGATCCCAAGCGGCAAGTCAATAGACGAGCGAGTGTGAT 810
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 468 RY.RD...B...RS.BSAYTNSG.CB.SSHCS.S.MNBS.H.BM.YM..M.KS.NT..M..409

QY 811 TCCCTTGATACATCTCAAGCACTTCTCTATGTTGAGTGTCTTACGCGCTGCTCAC 870
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N..349

QY 871 AATCAGAGCACTACCAAGATGTTTGGAGCTCTCTTCAAGCGCAGAGAGCGG 930
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A..289

QY 931 CCTGTGATGACCAAGCTCTTTGAGGTGACACTTGATGATGCTCTTGAAGAGAGA 990
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 288 TH.TNB...SNNMG.TG...TNRGY.GNCS.H.....N.NN.HH...MT.KNNR.R...229

QY 991 ACAACCAAGTCCCATATAGTAAC 1014
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 228 A.AS..BA.BTABNNMH.S.BM.M.205
```

RESULT 8
US-10-141-761-358/c

Sequence 358, Application US/10141761
Publication No. US20030148432A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Bilen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey

```
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C198  
CURRENT APPLICATION NUMBER: US/10/141,761  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 358  
LENGTH: 1049  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-141-761-358
```

Query Match 1.1%; Score 44.8; DB 15; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

```
QY 211 TCCCTGAACGAGGCAAGCACTTCTTCATGAGGCCCAAGCTCGCAACTGG 270
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1006 YMY...MSM...M.....BHBH.HK.Y.DS.R.T.M.N.AMTRMHAKB.BAMMS...947

QY 271 GTGGCCAAAGCCGACGCGGACCTGACAGCGCTTCGTCGCAAGAACTCCCCCGCC 330
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH.887

QY 331 GCTACTGCGCGCCCAAGATGGGCAATGGGCACTGTGTGTCGAGGTGCTTAATAGTT 390
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 886 S..Y.RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S...NA.H.GAR.H.S.827

QY 391 ATGGCACTCCCATATACACACAGGTCGAACTGTGGCAAGAACTTAAGCGCCCAAGT 450
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 826 .BS.CMDTC.CBGAHAT.R..AB.ADNBMWB.WBTHGAG..YND...KM.NN.BN...767

QY 451 GCGGTGCGCGCGCGCGCGCGCTGCTATGCGAGCGCTTGGACAAGTACGACTCGA 510
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 766 SAM..K..MNSH.H.RY...TH...RMA.SY..NNM...NM--SYGNS.Y..BAA..N.709

QY 511 TTGCTGATCCGCGCAAGCTGTGTAAGTCTGTCGCAAGGCTCTCTATTACGGC 570
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 708 DS.H.A..NM.G..MMMS.SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H...M..649

QY 571 GCGGCGATACCCCTTAAGTTCCCGCATCGAGTGAATACGGGTTCGAAGCAACTCTTC 630
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 648 NM...RYNHC.YW.BH.DNCY...AY.S.S.KAYSASS.HNHK.M..BM.NMA.N..589

QY 631 GAGAGTGAATCTCAATGAGTGCACCAAGCGCGCAAGGCAAGTGTCTATATGTT 690
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T....SCN.A.S..529

QY 691 GCGGTGCGCGCGCGCGCGCGCTGCTATGCGAGCGCTTGGACAAGTACCGCACTCGA 750
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK.ST.MMM.YGTYTRMH 469

QY 751 AGGCATGCCAATACAGAGATCCCAAGCGGCAAGTCAATAGACGAGCGAGTGTGAT 810
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 468 RY.RD...B...RS.BSAYTNSG.CB.SSHCS.S.MNBS.H.BM.YM..M.KS.NT..M..409

QY 811 TCCCTTGATACATCTCAAGCACTTCTCTATGTTGAGTGTCTTACGCGCTGCTCAC 870
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N..349

QY 871 AATCAGAGCACTACCAAGATGTTTGGAGCTCTCTTCAAGCGCAGAGAGAGCGG 930
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A..289
```

```
QY 931 CCTGTGATGCCAGCGCTTTGAGCTGACCTGATTGAGTCTCTAGCAAGAAGA 990
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TH.TNB....SNNMG.TG...TNRGY.GNCS.H.....N.NN.HH...MT.KXNR.R... 229

QY 991 ACAACCAAGTCCCATAGATAC 1014
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 A.AS..BA.BTABNNHM.S.BM.M 205

RESULT 9
US-10-142-885-358/c
; Sequence 358, Application US/10142885
; Publication No. US20030157604A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C248
; CURRENT APPLICATION NUMBER: US/10/142,885
; PRIOR FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-142-885-358

Query Match 1.1%; Score 44.8; DB 16; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTTGAAACGAGCAAGCAACTTCTTCATCGAGGCGCAAGCTCGAGTGAAGTGG 270
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1006 VNY...MGM...M.....BHM.HK.Y.DS.R.T.M.N.AMTRMHBK.BAMMS... 947

QY 271 GTGCCCAAGCCGAGCCGACCCCTGACGCTTCCGTGTCGAAGCACTCCCGCGCC 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BM.ABT.HMAHRB..THRGH. 887

QY 331 GGTACTGCGGCGCAACATGGGATTCGAGCTGTGTCTGAGAGTGTCTTAATAGTTT 390
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 886 S..Y.RCM.MTMG.DR.RWBHW.R.DSTAKKHK..SBS.S.S...NA.H..GAR.H.S 827

QY 391 ATGCACTCTCCCAATATACACACAGCTGCAAGCTTTGCGAGAAGCTTAAGCGCGCAAGT 450
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 826 .BS.CMDT.CBGAHAT.R.AB.ADNBWB.WBTHGAG..YND..KM.NN.BN... 767

QY 451 GGCCTGAGCGCGCCCAACTCTTACCAACCAAGCAAGATGAGCGCGCAATGTCAT 510
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 766 SAM..K..NNSS.H.RY...TH...RMA.SY..NNM...NM--..SYSNS.Y..BAA..N 709

QY 511 TTGCGTGAATCCGCGCAAGCGCTGTGATCGTCTGCGACAGGTCTCTTAATTCAGCGC 570
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 708 DS.H.A..NM.G..MMMS.SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H....M.. 649
```

```
QY 571 GCGGCAATACCCCTTAAGTCCCGCATCGAGTACGAGTATCCAGTTCACCAAGCATCTCTC 630
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 648 NM...RTHNC.YW.BH.DNCT..AY.S.S.KAYSASSS.HNHKK.M..BM.NMA.N. 589

QY 631 GAGAGTGAATCTCAATCACTGACGACCAAGCGGCGCAAGGCGCAAGCTGTCTGATATGTT 690
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T.....SCN.A.S. 529

QY 691 GCGGCTGCGCGCGCGCGCGCGCGCTGCTATTTGAGAGCGCTTTGAGACAAGTACCGACTGCA 750
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK.ST.NM.YGSYTRMH 469

QY 751 AGGCATGCCAATACAGAGATCCACGCGCAGAGTCTAAGCAGCGGACCGAGCGTGGAT 810
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 468 RY.RD....B...RS.BSAYTNSG.CB.SHSKS.S.NMBS.H.BM.YM..M.KS.NT.M. 409

QY 811 TCCTTGATACATCTCAAGGCACTTCTATGTTGAGTGTCTTCAAGCGCTTCCGCTCAC 870
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB....N. 349

QY 871 AATCAGACGACATCCCAAGATGATTGAGGCTCTCTTACAGCCGACGAGAGAAGCGG 930
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 348 S.H...S...D..MTHC..MT..N.S.H...NM.NM.WY..BD..SNSD.Y.BM..A. 289

QY 931 CCTGTGATGCCAGCGCTTTGAGCTGACACTTGATTTGAGTCTCTAGCAAGAAGA 990
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 TH.TNB....SNNMG.TG...TNRGY.GNCS.H.....N.NN.HH...MT.KXNR.R... 229

QY 991 ACAACCAAGTCCCATAGATAC 1014
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 228 A.AS..BA.BTABNNHM.S.BM.M 205
```

```
RESULT 10
US-10-158-790-358/c
; Sequence 358, Application US/10158790
; Publication No. US20030180879A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C448
; CURRENT APPLICATION NUMBER: US/10/158,790
; PRIOR FILING DATE: 2002-05-30
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-158-790-358

Query Match 1.1%; Score 44.8; DB 16; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTTGAAACGAGCAAGCAACTTCTTCATCGAGGCGCAAGCTCGAGTGAAGTGG 270
```

```

Db      1006 YMY...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTRHAB.BAMMS...947
QY      271 GTGCCCAAGCCGACCGGACCTTGACAGCTTCGTCGACGAGAACCTCCCGCGC 330
Db      946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH..887
QY      331 GCTACTGCCGCGCAACATGGGCACTTGCACTGTGTGCTCAGAGGCTTAATAGTT 390
Db      886 S..Y.RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S...NA.H..GAR.H.S 827
QY      391 ATGCCACCTCCCAATACACACAGGTCGACAGCTTTGGCAGAACTTAAGCGGCCCAAGT 450
Db      826 .BS.CMDTC.CBGBHAT.R..AB.ADNBWB.WBTHAG..YND..KM.NN.BN...767
QY      451 GGCCTAGCGCGCAACCTTACCAACCAAGGAGAGTACCGCGCCCAATGTCTACT 510
Db      766 SAM..K..MNS.H.RV...TH...RMA.SY..NNM...NM--..SYSGNS.Y..BAA..N 709
QY      511 TTGCGTATCGCGCCCAAGCGCTGTGACGCTGCTGCGCAGAGTCTCTTATTCAGCGC 570
Db      708 DS.H.A..NM.G..MMMS..SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H...M..649
QY      571 GCGGCGATACCCCTAAAGTCCCGGACGATCCAGTATACGGGTCCAAAGCACCATCTCTC 630
Db      648 NM...RYNHC.YM.BH.DNCT...AY.S.S.KAYSASS.HNHKK.M..BM.NMA.N..589
QY      631 GAGAGTGAAGATCTCAATCAGTACGACCAAGCGGCGCAAGGCAAGCTGTCTGATTAATGTT 690
Db      588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RV..T....SCN.A.S..529
QY      691 GCGCGTCCGCGCGCGCGCGCGCGCTTATTCGAGCGCTTGACAGGAGTACGACTCGA 750
Db      528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CNRKGS.NBSK..ST.NMM.YGSTRBH 469
QY      751 AGCGATGCCAATACGAGATCCGCGGACGATCATGACGAGCGGACGAGTGAT 810
Db      468 RY.RD...B..RS.BSAYTNSG.CB.SSHCS.S.MNBS.H.BM.YM..M.KS.NT..M..409
QY      811 TCGTTGATATCATCTCAAGGCACTTCTATGTTGATGCTCTTCAAGCGTTCGCTGAC 870
Db      408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTRB...N..349
QY      871 AATCAGAGCACTACCAAGAGTATTGAGGCTCTCTTCAAGCCCAAGAGAAAGCG 930
Db      348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A..289
QY      931 CCTGTGATGCCAGGCTTTGAGGCTGAGCACTTGATGAGTCTCTAGCAAGAGAGA 990
Db      288 TH.TNB...SNMNG.TG...TNRGY.GNCS.H...N.NN.HH...MT.KNNR.R...229
QY      991 ACAACCAAGTCCCATAGATAAC 1014
Db      228 A.AS..BA.BTANNM.S.BM.M 205

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RESULT 11
US-10-137-871-358/c
Sequence 358, Application US/10137871
Publication No. US20030207350A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Godard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria

```

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C15
CURRENT APPLICATION NUMBER: US/10/137,871
Prior Application removed - 2002-05-03
Prior Application removed - See Palm or File Wrapper
SEQUENCE OF SEQ ID NOS: 550
SEQ ID NO 358
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-871-358

Query Match      1.1%; Score 44.8; DB 17; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0045;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY      211 TCCCTGAACAGCAGAGCCCACTTCTCATCGAGGCGCAAGCTGCGCATCGAGCTG 270
Db      1006 YMY...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTRHAB.BAMMS...947
QY      271 GTGCCCAAGCCGACCGGACCTTGACAGCTTCGTCGACGAGAACCTCCCGCGC 330
Db      946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH..887
QY      331 GCTACTGCCGCGCAACATGGGCACTTGCACTGTGTGCTCAGAGGCTTAATAGTT 390
Db      886 S..Y.RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S...NA.H..GAR.H.S 827
QY      391 ATGCCACCTCCCAATACACACAGGTCGACAGCTTTGGCAGAACTTAAGCGGCCCAAGT 450
Db      826 .BS.CMDTC.CBGBHAT.R..AB.ADNBWB.WBTHAG..YND..KM.NN.BN...767
QY      451 GGCCTAGCGCGCAACCTTACCAACCAAGGAGAGTACCGCGCCCAATGTCTACT 510
Db      766 SAM..K..MNS.H.RV...TH...RMA.SY..NNM...NM--..SYSGNS.Y..BAA..N 709
QY      511 TTGCGTATCGCGCCCAAGCGCTGTGACGCTGCTGCGCAGAGTCTCTTATTCAGCGC 570
Db      708 DS.H.A..NM.G..MMMS..SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H...M..649
QY      571 GCGGCGATACCCCTAAAGTCCCGGACGATCCAGTATACGGGTCCAAAGCACCATCTCTC 630
Db      648 NM...RYNHC.YM.BH.DNCT...AY.S.S.KAYSASS.HNHKK.M..BM.NMA.N..589
QY      631 GAGAGTGAAGATCTCAATCAGTACGACCAAGCGGCGCAAGGCAAGCTGTCTGATTAATGTT 690
Db      588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RV..T....SCN.A.S..529
QY      691 GCGCGTCCGCGCGCGCGCGCGCTTATTCGAGCGCTTGACAGGAGTACGACTCGA 750
Db      528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRKGS.NBSK..ST.NMM.YGSTRBH 469
QY      751 AGCGATGCCAATACGAGATCCGCGGACGATCATGACGAGCGGACGAGTGAT 810
Db      468 RY.RD...B..RS.BSAYTNSG.CB.SSHCS.S.MNBS.H.BM.YM..M.KS.NT..M..409
QY      811 TCGTTGATATCATCTCAAGGCACTTCTATGTTGATGCTCTTCAAGCGTTCGCTGAC 870
Db      408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTRB...N..349
QY      871 AATCAGAGCACTACCAAGAGTATTGAGGCTCTCTTCAAGCCCAAGAGAAAGCG 930
Db      348 S.H...S...D..MTHC..MT..N.S.H...MN.NM.WY..BD..SNSD.Y.BM..A..289
QY      931 CCTGTGATGCCAGGCTTTGAGGCTGAGCACTTGATGAGTCTCTAGCAAGAGAGA 990
Db      288 TH.TNB...SNMNG.TG...TNRGY.GNCS.H...N.NN.HH...MT.KNNR.R...229

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QY 991 ACAACCAAGTCCCATATGATAC 1014
| : : : : :
DB 228 A.AS..BA.BTANNHM.S.BM.M 205

RESULT 12

US-10-140-923-358/c
; Sequence 358, Application US/10140923
; Publication No. US20030207355A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C188
CURRENT APPLICATION NUMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 358
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-923-358

Query Match 1.1%; Score 44.8; DB 17; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTTAACCAAGCCAGCAAGCACTTTCATGAGAGCCCAAGAGCTGCGAGCTG 270
| : : : : :
DB 1006 YMT...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTMHAKB.BAMMS... 947
QY 271 GTGCCCAAGCCCAAGCCGACCTTCCGTCGTCGAAGCAAGCTCCCGCGCC 330
| : : : : :
DB 946 S.S.N..B..C..MHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAIRB..THRGH.. 887
QY 331 GCTACTGCGGCGCAACAGTGGGATTCGACAGCTGTTGCTGAGGTGCTTAATAGTTT 390
| : : : : :
DB 886 S..Y..RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S....NA.H..GAR.H.S. 827
QY 391 ATGCCACCTCCCAATAACACACAGAGTTCGAGAGCTTGGCAAGCTTAAGCGGCCCAAGT 450
| : : : : :
DB 826 .BS.CMDTC.CBGBAHAT.R..AB.ADNBWB.WBTHGAG..YND...KM.NN..BN... 767
QY 451 GGCCTAGCGCCCACTTCAACCAACCAAGAGAGCGCCCAATGTCAC 510
| : : : : :
DB 766 SAM..K..MNS.S.H.RY...TH...RMA..SY..NNM...NM...SYSGNS.Y..BAA..N. 709
QY 511 TTGCTGATCCGCCCAAGCGTGTGACTGCTGCGACAGAGTCTCTTATTCAGCGC 570
| : : : : :
DB 708 DS.H.A..NM.G..MMMS..SM..CMNT.S..NM..N..KCH..BCS...S.SNMS.H...M.. 649
QY 571 GCGGATATCCCTTAAGTTCCCGGATCCAGTGAATATACGGGTCCAAAGACATCTGC 630
| : : : : :
DB 648 NM...RYNHC.YW.BH.DNCY...AY.S.S..KAYSASS.S.HMHKK..M..BM.NMA..N.. 589

QY 631 GAGAGTGAATCTCATGATGACCAAGCGGCCCAAGGCAAGCTGTCTGATATGTT 690
| : : : : :
DB 588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T.....SCN.A.S. 529
QY 691 GCGGTCGCGCGCGCGCGCGCGCTTATTCGAGCGCTTGGACAGTACCGACTGA 750
| : : : : :
DB 528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK..ST..MM.YGSYTBW 469
QY 751 AGCGATGCCAATAGACAGAGATCCACGGGACAGATCATAGACGAGCGGACCGATGAT 810
| : : : : :
DB 468 RY.RD...B...RS.BSAYTNSG..CB..SSHOS.S.MBS.H.BM.YM..M.KS..NT..M. 409
QY 811 TCCTTGAATCATCTCAAGGCACTTCTATGATGTCGATGCGCTTCCGCTGAC 870
| : : : : :
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N. 349
QY 871 AATCAGACACTAACCAAGTATGTTTGAAGCTCTCTTCAACAGCCAGAGAGAGCGG 930
| : : : : :
DB 348 S.H...S...D..MTHC..MT..N.S.H...NM.NM.WY..BD..SNSD.Y..BM..A. 289
QY 931 CCGTGATGACGAGCTGTTGAGGCTGACACTTGAATGATTCCTTACGAAGAAGA 990
| : : : : :
DB 288 TH.TNB...SNMG.TG...TNRGY.GNCS.H.....N..NN..HH...MT.KNNR.R... 229
QY 991 ACAACCAAGTCCCATATGATAC 1014
| : : : : :
DB 228 A.AS..BA.BTANNHM.S.BM.M 205

RESULT 13

US-10-141-756-358/c
; Sequence 358, Application US/10141756
; Publication No. US20030207359A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C200
CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 358
LENGTH: 1049
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-756-358

Query Match 1.1%; Score 44.8; DB 17; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTGAACAGGAGCAAGCACTTTCATGAGAGCCCAAGAGCTGCGAGCTGCAACTGG 270
| : : : : :
DB 1006 YMT...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTMHAKB.BAMMS... 947
QY 271 GTGCCCAAGCCCAAGCCGACCTTCCGTCGTCGAAGCAAGCTCCCGCGCC 330
| : : : : :
DB 946 YMT...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTMHAKB.BAMMS... 947

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Db      946 S.S.N..B..C..MHY...G.N..DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH..887
QY      331 GCTACTGCGCGCAACAATGGGCAATTCGACAGTGTGTTGTCAGAGTGTATATAGTTT 390
Db      886 S..Y..RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S....NA.H..GAR.H.S.827
QY      391 ATGCCACCTCCCAATAACACACAGGCGGAAGCTTTGGCAAGAACTCTTAAGCGGCCAAGT 450
Db      826 .BS.CMDTC.CBGAHAT..R..AB..ADNBWB..WBTHGAG..YND..KM.NN..BN...767
QY      451 GGCCTGAGCGCGCAACCTTACCAACCAACCAAGGAGAGCGCGCAATGCTACT 510
Db      766 SAM..K..MNS.S.H.RY..TH...RMA.SY..NNM...NM--..SYSNS.Y..BAA..N.709
QY      511 TTGCTGATCCGCCCAAGCGCTGTGACTGCTGCGCAAGGCTCTCTTATTCAGCGC 570
Db      708 DS.H.A..NM.G..MMWS..SM..CNMT.S..NM.N..KCH..BCS...S.SNMS.H....M..649
QY      571 GCGGCAATACCCCTTAAGTTCCCGATTCAGTAATCCGTTCCAAAGCAATCTCTC 630
Db      648 NM...RYNHC.YW.BH.DNCY...AY.S.S..KAYSASS.HNHNK.M..BM.NMA.N..589
QY      631 GAGAGTGAATCTCAATGACGACCAAGCGGCAAGGCAAGCTGTGATATGTT 690
Db      588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T....SCN.A.S..529
QY      691 GCGGCTGCGCGCGCGCGCGCGCTGCTTATTCAGGCGCTTGGACAAGTACGACTGA 750
Db      528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS..NBSK..ST..MMM.YGSYTRMH 469
QY      751 AGGCAATGCCAATCGAGAGATCCCAAGCGGCAAGCTCATAGAGCGGCAAGTGGAT 810
Db      468 RY.RD...B...RS..BSAYTNSG..CB.SSHCS.S..MNB.S.H..BM.YM..M.KS..NT..M..409
QY      811 TCCTTGATATCATCTCAAGGCACTTCTTATGATGTTGAGTGTCTTCAAGCGCTGAC 870
Db      408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N..349
QY      871 AATCAGAGCACTAACCAAGATGTTTGAAGCTCTCTTACAGCGGCAAGAGAGCGG 930
Db      348 S.H....S...D..MTHC..MT..N.S.H....MN.NM.WY..BD..SNSD.Y.BM..A..289
QY      931 CCTGTGATGCCACGCTCTTGAAGCTGACACTTGAATGAGTCTCTTACGAAGAAGA 990
Db      288 TH.TNB....SNNG..TG...TNRGY.GNCS.H....N.NN.HH...MT..KNNR.R...229
QY      991 ACAACCAAGTCCACATAGATAAC 1014
Db      228 A..AS..BA..BTABNNHM.S.BM.M.205

RESULT 14
US-10-141-759-358/c
; Sequence 358, Application US/10141759
; Publication No. US20030207361A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltzen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guiney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
```

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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C197
; CURRENT APPLICATION NUMBER: US/10/141,759
; PRIOR APPLICATION DATE: 2002-05-08
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRP
; ORGANISM: Homo Sapien
US-10-141-759-358

Query Match      1.1%, Score 44.8; DB 17; Length 1049;
Best Local Similarity 5.2%; Pred. No. 0.0049;
Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY      211 TCCTGGAACGAGGCAAGCAACTTCTTCATCGAGGCGCAAGCTGCGAGTCTGAACTGG 270
Db      1006 YMT...MSM..M.....BHM.HK.Y.DS.R.T.M.N.AMTRMHKB.BAMWS...947
QY      271 GTGCCCAAGCCGACGCGGCAAGCTTCCGCTGCAAGAACTCCCGCGCC 330
Db      946 S.S.N..B..C..WHY...G.N.DM.Y.H..MTB..T.BW.ABT.HMAHRB..THRGH..887
QY      331 GCTACTGCGCGCAACAATGGGCAATTCGACAGTGTGTTGTCAGAGTGTATATGTTT 390
Db      886 S..Y..RCM.MTWG.DR.RWBHW.R.DSTAKBK...SBS.S.S....NA.H..GAR.H.S.827
QY      391 ATGCCACCTCCCAATAACACACAGGCGGAAGCTTTGGCAAGAACTCTTAAGCGGCCAAGT 450
Db      826 .BS.CMDTC.CBGAHAT..R..AB..ADNBWB..WBTHGAG..YND..KM.NN..BN...767
QY      451 GGCCTGAGCGCGCAACCTTACCAACCAACCAAGAGAGAGCGCGCAATGCTACT 510
Db      766 SAM..K..MNS.S.H.RY..TH...RMA.SY..NNM...NM--..SYSNS.Y..BAA..N.709
QY      511 TTGCTGATCCGCCCAAGCGCTGTGACTGCTGCGCAAGGCTCTCTTATTCAGCGC 570
Db      708 DS.H.A..NM.G..MMWS..SM..CNMT.S..NM.N..KCH..BCS...S.SNMS.H....M..649
QY      571 GCGGCAATACCCCTTAAGTTCCCGATTCAGTAATCCGTTCCAAAGCAATCTCTC 630
Db      648 NM...RYNHC.YW.BH.DNCY...AY.S.S..KAYSASS.HNHNK.M..BM.NMA.N..589
QY      631 GAGAGTGAATCTCAATGACGACCAAGCGGCAAGGCAAGCTGTGATATGTT 690
Db      588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNNS.H.RY..T....SCN.A.S..529
QY      691 GCGGCTGCGCGCGCGCGCGCGCTGCTTATTCAGGCGCTTGGACAAGTACGACTGA 750
Db      528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS..NBSK..ST..MMM.YGSYTRMH 469
QY      751 AGGCAATGCCAATCGAGAGATCCCAAGCGGCAAGTCAATAGCAGCGGCAAGAGTGA 810
Db      468 RY.RD...B...RS..BSAYTNSG..CB.SSHCS.S..MNB.S.H..BM.YM..M.KS..NT..M..409
QY      811 TCCTTGATATCATCTCAAGGCACTTCTTATGATGTTGAGTGTCTTCAAGCGCTGAC 870
Db      408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N..349
QY      871 AATCAGAGCACTAACCAAGATGTTTGAAGCTCTCTTACAGCGGCAAGAGAGCGG 930
Db      348 S.H....S...D..MTHC..MT..N.S.H....MN.NM.WY..BD..SNSD.Y.BM..A..289
QY      931 CCTGTGATGCCACGCTCTTGAAGCTGACACTTGAATGAGTCTCTTACGAAGAAGA 990
Db      288 TH.TNB....SNNG..TG...TNRGY.GNCS.H....N.NN.HH...MT..KNNR.R...229
QY      991 ACAACCAAGTCCACATAGATAAC 1014
Db      228 A..AS..BA..BTABNNHM.S.BM.M.205
```

RESULT 15

US-10-140-805-358/c
; Sequence 358, Application US/10140805
; Publication No. US20030207417A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey E.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matarabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C176
; CURRENT APPLICATION NUMBER: US/10/140,805
; PRIORITY FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 358
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-805-358

Query Match 1.1%; Score 44.8; DB 17; Length 1049;
Best local Similarity 5.2%; Pred. No. 0.0049;

Matches 42; Conservative 229; Mismatches 531; Indels 2; Gaps 1;

QY 211 TCCTGACCGAGAGAGCACTTCTTCATGAGGCCAAGCTGCGAGCTGCACTG 270
DB 1006 YMY...MSM...M.....BHM.HK.Y.DS.R.T.M.N.AMTMHAJB.BAMMS... 947
QY 271 GTGCCCAAGCCCGACCCGACCTTGACAGCTTCCGTGTCACAGAACCTCCCGCCG 330
DB 946 S.S.N..B..C..WHY..G.N.DM.Y.H..MTB..T.BM.ABT.HMAHRB..THRGH. 887
QY 331 GCTACTGCCGCGCAACATGGGATGACAGCTGTGCTGCGAGGTGCTTAATAGTTT 390
DB 886 S..Y.RCM.MTWG.DR.RWBHW.R.DSTAKBK..SBS.S.S...NA.H.GAR.H.S. 827
QY 391 ATGCCACTTCCCAATACACACCCAGGTGCAAGCTTTGGCAAGACTTAAGCGCCCAAGT 450
DB 826 .BS.CMDTC.CBGAHBAT.R..AB.ADNBMBW.BPTHGAG..YND..KM.NN..BN... 767
QY 451 GGCCTGAGCGCGCCACTTACCAACCAAGCAAGATGAGCGCCGCAATGTCACT 510
DB 766 SAM..K..MNSS.H.RY..TH...RMA.SY..NNM..NM--SYGNS.Y..BAA..N 709
QY 511 TTGCTGATCCGCGCAAGCTGTGACTCGCTGCGCAAGGTCTCTTAATTCACGCGC 570
DB 708 DS.H.A..NM.G..MMMS..SM.CNMT.S.NM.N..KCH.BCS...S.SNMS.H...M.. 649
QY 571 GCGGCGATACCCCTAAAGTTCCCGATCCAGTGAATACCGGTTCCAAAGCAACCATCTTC 630
DB 648 NM...RYNHC.YM..BH.DNCY...AY.S.S.KAYSASS.HHNKK.M..BM.NMA..N. 589
QY 631 GAGAGTGAATCTCAATGACGACCAAGCGCGCCCAAGGCAAGTGTCTGATATGTT 690
DB 588 KDA.C.S..RDSNS.H.B..MD...TASD..H.YNS.H.RY..T.....SCN.A.S. 529

QY 691 GCCGTGCGCGCGCCCGCGCTGCTTAATGAGAGCGCTTGGACAGATACCACTGCA 750
DB 528 .NCS.N.GM..S.D..HSSMB...SNMS.H.A.CMRGS.NBSK.ST.MNM.YGSYTMH 469
QY 751 AGCATGCCAATACGAGAGATCCACGCGCAGAGTCAATAGACGCGAGCAGGTGAT 810
DB 468 RX.RD...B...RS.BSAYTNSG.CB.SSHCS.S.MNBS.H.BM.YM..M.KS.NT.M. 409
QY 811 TCCTTGATACATCTCAAGGCACTTCTATGAGTGTGAGAGTCTTCAAGCGCTTCCGCTAC 870
DB 408 .NAC.H.B..N..ND..S.N.SM..M.BRCY.Y..M.SM.SS.T.S.NKSTYRB...N. 349
QY 871 AATCAGAGCACTACCCAGAGTAGTTTGGAGGCTCTCTTACAGCCAGAGAGAGCGG 930
DB 348 S.H...S...D..MTHC.MT..N.S.H...NM.NM.WY..BD..SNSD.Y.BM..A. 289
QY 931 CCTGTGATGCCAGCGCTTTGAGGCTGAGACCTGATTAAGTCTCTTACCAAGAAAGA 990
DB 288 TH.TNB...SNNMG.TG...TNRGY.GNCS.H.....N.NN..HH...MT.KNNR.R.. 229
QY 991 ACAACCAAGTCCACATAGATAAC 1014
DB 228 A.AS..BA.BTABNNHM.S.BM.M 205

Search completed: September 7, 2005, 10:28:01
Job time : 25393 secs